

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/290,798

DATE: 10/30/2001  
 TIME: 11:50:45

Input Set : N:\Crf3\RULE60\09290798.txt  
 Output Set: N:\CRF3\10302001\I290798.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:  
 5 (i) APPLICANT: Hellstrom, Ingegerd  
 6 Hellstrom, Karl E  
 7 Bruce, Kim F  
 8 Schreiber, George  
 10 (ii) TITLE OF INVENTION: Novel Antibody Conjugates Reactive with  
 11 Human Carcinomas  
 13 (iii) NUMBER OF SEQUENCES: 4  
 15 (iv) CORRESPONDENCE ADDRESS:  
 16 (A) ADDRESSEE: Sheldon & Mak  
 17 (B) STREET: 225 South Lake Avenue, Ninth Floor  
 18 (C) CITY: Pasadena  
 19 (D) STATE: California  
 20 (E) COUNTRY: USA  
 21 (F) ZIP: 91101  
 23 (v) COMPUTER READABLE FORM:  
 24 (A) MEDIUM TYPE: Floppy disk  
 25 (B) COMPUTER: IBM PC compatible  
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  
 29 (vi) CURRENT APPLICATION DATA:  
 C--> 30 (A) APPLICATION NUMBER: US/09/290,798  
 C--> 31 (B) FILING DATE: 05-Apr-1999  
 32 (C) CLASSIFICATION:  
 35 (vii) PRIOR APPLICATION DATA:  
 36 (A) APPLICATION NUMBER: 08/077,253  
 37 (B) FILING DATE: 14-JUN-1993  
 40 (viii) ATTORNEY/AGENT INFORMATION:  
 41 (A) NAME: Adriano, Sarah B.  
 42 (B) REGISTRATION NUMBER: 34,470  
 43 (C) REFERENCE/DOCKET NUMBER: 7004-2  
 45 (ix) TELECOMMUNICATION INFORMATION:  
 46 (A) TELEPHONE: (818) 796-400  
 47 (B) TELEFAX: (818) 795-6321  
 50 (2) INFORMATION FOR SEQ ID NO: 1:  
 52 (i) SEQUENCE CHARACTERISTICS:  
 53 (A) LENGTH: 33 base pairs  
 54 (B) TYPE: nucleic acid  
 55 (C) STRANDEDNESS: single  
 56 (D) TOPOLOGY: linear  
 58 (ii) MOLECULE TYPE: DNA (genomic)  
 60 (iii) HYPOTHETICAL: NO  
 62 (iv) ANTI-SENSE: NO  
 64 (vi) ORIGINAL SOURCE:  
 65 (A) ORGANISM: Plasmid pBR96  
 68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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70 GCTAGACATA TGGAGGTGCA GCTGGTGGAG TCT 33
72 (2) INFORMATION FOR SEQ ID NO: 2:
74     (i) SEQUENCE CHARACTERISTICS:
75         (A) LENGTH: 33 base pairs
76         (B) TYPE: nucleic acid
77         (C) STRANDEDNESS: single
78         (D) TOPOLOGY: linear
80     (ii) MOLECULE TYPE: DNA (genomic)
82     (iii) HYPOTHETICAL: NO
84     (iv) ANTI-SENSE: NO
86     (vi) ORIGINAL SOURCE:
87         (A) ORGANISM: Plasmid pBR96
90     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
92 GCTGTGGAGA CTGGCCTGGT TTCTGCAGGT ACC 33
94 (2) INFORMATION FOR SEQ ID NO: 3:
96     (i) SEQUENCE CHARACTERISTICS:
97         (A) LENGTH: 720 base pairs
98         (B) TYPE: nucleic acid
99         (C) STRANDEDNESS: single
100        (D) TOPOLOGY: linear
102     (ii) MOLECULE TYPE: DNA (genomic)
104     (iii) HYPOTHETICAL: NO
106     (iv) ANTI-SENSE: NO
108     (vi) ORIGINAL SOURCE:
109         (A) ORGANISM: Mus musculus
111     (ix) FEATURE:
112         (A) NAME/KEY: CDS
113         (B) LOCATION: 1..720
116     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
118 ATG GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTA GTG CAG CCT GGG 48
119 Met Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
120 1 5 10 15
122 TCC CTG AAA GTC TCC TGT GTA ACC TCT GGA TTC ACT TTC AGT GAC TAT 96
123 Ser Leu Lys Val Ser Cys Val Thr Ser Gly Phe Thr Phe Ser Asp Tyr
124 20 25 30
126 TAC ATG TGG GTT CGC CAG ACT CCA GAG AAG AGG CTG GAG TGG GTC GCA 144
127 Tyr Met Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala
128 35 40 45
130 TAC ATT AGT CAA GGT GAT ATA ACC GAC TAT CCA GAC ACT GTA AAG GGT 192
131 Tyr Ile Ser Gln Gly Asp Ile Thr Asp Tyr Pro Asp Thr Val Lys Gly
132 50 55 60
134 CGA TTC ACC ATC TCC AGA GAC AAT AAG AAC ACC CTG TAC CTG CAA ATG 240
135 Arg Phe Thr Ile Ser Arg Asp Asn Lys Asn Thr Leu Tyr Leu Gln Met
136 65 70 75 80
138 AGC CGT CTG AAG TCT GAG GAC ACA GCC ATG TAT TGT GCA AGA GGC CTG 288
139 Ser Arg Leu Lys Ser Glu Asp Thr Ala Met Tyr Cys Ala Arg Gly Leu
140 85 90 95
142 GAC GAC GGG GCC TGG TTT GCT TAC TGG GGC CAA GGG ACC ACG ACC GTC 336
143 Asp Asp Gly Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr Thr Thr Val

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144          100          105          110
146 TCC TCA GGA TCC GGA GGT GGA GGT TCT GGT GGA GGT GGA TCT GGA GGT      384
147 Ser Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
148          115          120          125
150 GGA TCT AAG CTT GAT GTT TTG ATG ACC CAA ATT CCA GTC TCC CTG CCT      432
151 Gly Ser Lys Leu Asp Val Leu Met Thr Gln Ile Pro Val Ser Leu Pro
152          130          135          140
154 GTC AGT CTT GGA CAA GCG TCC ATC TCT TGC AGA TCT AGT CAG ATC ATT      480
155 Val Ser Leu Gly Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ile Ile
156 145          150          155          160
158 GTA CAT AAT AAT GGC AAC ACC TTA GAA TGG TAC CTG CAG AAA CCA GGC      528
159 Val His Asn Asn Gly Asn Thr Leu Glu Trp Tyr Leu Gln Lys Pro Gly
160          165          170          175
162 CAG TCT CCA CAG CTC CTG ATC TAC AAA GTT AAC CGA TTT TCT GGG GTC      576
163 Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Asn Arg Phe Ser Gly Val
164          180          185          190
166 CCA GAC AGG TTC AGC GGC AGT GGA TCA GGG ACA GAT TTC CTC AAG ATC      624
167 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Leu Lys Ile
168          195          200          205
170 AGC AGA GTG GAG GCT GAG GAT CTG GGA GTT TAT TAC TGC TTT CAA GTT      672
171 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Val
172          210          215          220
174 CAT GTT CCA TTC ACG TTC GGC TCG GGG ACC AAG CTG GAG ATC AAA CGC      720
175 His Val Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
176 225          230          235          240
179 (2) INFORMATION FOR SEQ ID NO: 4:
181   (i) SEQUENCE CHARACTERISTICS:
182       (A) LENGTH: 240 amino acids
183       (B) TYPE: amino acid
184       (D) TOPOLOGY: linear
186   (ii) MOLECULE TYPE: protein
188   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
190 Met Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
191   1          5          10          15
193 Ser Leu Lys Val Ser Cys Val Thr Ser Gly Phe Thr Phe Ser Asp Tyr
194          20          25          30
196 Tyr Met Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val Ala
197          35          40          45
199 Tyr Ile Ser Gln Gly Asp Ile Thr Asp Tyr Pro Asp Thr Val Lys Gly
200          50          55          60
202 Arg Phe Thr Ile Ser Arg Asp Asn Lys Asn Thr Leu Tyr Leu Gln Met
203   65          70          75          80
205 Ser Arg Leu Lys Ser Glu Asp Thr Ala Met Tyr Cys Ala Arg Gly Leu
206          85          90          95
208 Asp Asp Gly Ala Trp Phe Ala Tyr Trp Gly Gln Gly Thr Thr Val
209          100          105          110
211 Ser Ser Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
212          115          120          125
214 Gly Ser Lys Leu Asp Val Leu Met Thr Gln Ile Pro Val Ser Leu Pro

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215	130	135	140
217	Val Ser Leu Gly Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ile Ile		
218	145	150	155
220	Val His Asn Asn Gly Asn Thr Leu Glu Trp Tyr Leu Gln Lys Pro Gly		
221		165	170
223	Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Asn Arg Phe Ser Gly Val		
224		180	185
226	Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Leu Lys Ile		
227		195	200
229	Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Val		
230	210	215	220
232	His Val Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg		
233	225	230	235
			240

VERIFICATION SUMMARY

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]